

Donde

STIC Biotechnology Systems Branch

STIC

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

Source:

Date Processed by STIC:

10/049,967C
PCT
6/2/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office; and instead should be sent via the following to the indicated addresses

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - cPAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

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Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/049,967

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY FTO SOFTWARE

1. Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2. Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
3. Missigned Amino Numbering The numbering under each 5' amino acid is missigned. Do not use tab codes between numbers; use space characters, instead.
4. Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5. Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6. PatentIn 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7. Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)
(ii) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped.

Please also adjust the "(iii) NUMBER OF SEQUENCES" response to include the skipped sequence.
8. Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000
9. Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa and which residue n or Xaa represents.
10. Invalid <21> Response Per 1.823 of Sequence Rules, the only valid <21> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <21> response is Unknown or is Artificial Sequence.
11. Use of <220> Sequence(s) missing the <220> feature and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <21> "Organism" response is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (See 1.823 of Sequence Rules)
12. PatentIn 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13. Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid.

AMC - Biotechnology Systems Branch - 09/09/2003

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PCT

RAW SEQUENCE LISTING

DATE: 06/02/2005

PATENT APPLICATION: US/10/049,967C

TIME: 08:23:10

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\06022005\J049967C.raw

2 <110> APPLICANT: Imperial College Innovations Limited
 W--> 3 <120> TITLE OF INVENTION: Isoforms of Snare Molecules and the Uses Thereof in
 W--> 4 Modulation of Cellular Exocytosis
 W--> 5 <130> FILE REFERENCE: ICOY/P23294PC
 W--> 6 <140> CURRENT APPLICATION NUMBER: US/10/049,967C
 7 <141> CURRENT FILING DATE: 2002-02-18
 W--> 8 <160> NUMBER OF SEQ ID: 28
 9 <170> SOFTWARE: PatentIn Ver. 2.0

ERRORED SEQUENCES

26 <210> SEQ ID NO: 3
 27 <211> LENGTH: 29 - Found 28
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Artificial Sequence
 W--> 30 <220> FEATURE:
 31 <223> OTHER INFORMATION: Description of Artificial Sequence: pcr primer
 W--> 32 <400> SEQUENCE: 3
 E--> 33 catcttggtt gaagctgcgt tggcttcat (29) - 28
 34 <210> SEQ ID NO: 4
 35 <211> LENGTH: 30 - Found 29
 36 <212> TYPE: DNA
 37 <213> ORGANISM: Artificial Sequence
 W--> 38 <220> FEATURE:
 39 <223> OTHER INFORMATION: Description of Artificial Sequence: pcr primer
 W--> 40 <400> SEQUENCE: 4 30 delete
 E--> 41 catcttggtt gctttgcgt tggcttcat (29) - 28
 42 <210> SEQ ID NO: 5
 43 <211> LENGTH: 32 - Found 31
 44 <212> TYPE: DNA
 45 <213> ORGANISM: Artificial Sequence
 W--> 46 <220> FEATURE:
 47 <223> OTHER INFORMATION: Description of Artificial Sequence: pcr primer
 W--> 48 <400> SEQUENCE: 5
 E--> 49 agcatcttg ttgcccacca gttggettda (32) - 31
 162 <210> SEQ ID NO: 20
 163 <211> LENGTH: 10
 164 <212> TYPE: PRT
 165 <213> ORGANISM: Homo Sapiens
 168 <400> SEQUENCE: 20
 169 Gln Arg Ala Thr Lys Met Leu Gly Ser Gly
 E--> 170 1 1 5 8 10 10

Does Not Comply
 Corrected Diskette Needed
 (Pg. 1-2)

pls group amino acids
 in sets of 10s

FOR ex 2

atgctgtgc a aatgtgctc 20

pls group amino
 acids in sets of
 10s. FOR ex 2

aatgtgctat attcggta

RAW SEQUENCE LISTING

DATE: 06/02/2005

PATENT APPLICATION: US/10/049,967C

TIME: 08:23:10

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\06022005\J049967C.raw

171 <210> SEQ ID NO: 21
172 <211> LENGTH: 10
173 <212> TYPE: PRT
174 <213> ORGANISM: Artificial Sequence
W--> 175 <220> FEATURE:
176 <223> OTHER INFORMATION: Description of Artificial Sequence: synthesized
W--> 177 <400> SEQUENCE: 21
178 Gln Thr Ala Thr Lys Met Leu Gly Ser Gly
E--> 179 1 1 5 5 10 10
216 <210> SEQ ID NO: 26
217 <211> LENGTH: 5
218 <212> TYPE: PRT
219 <213> ORGANISM: Artificial Sequence
W--> 220 <220> FEATURE:
221 <223> OTHER INFORMATION: Description of Artificial Sequence: synthesized
224 <400> SEQUENCE: 26
225 Gln Arg Ala Thr Lys
E--> 226 1 1 5 5
227 <210> SEQ ID NO: 27
228 <211> LENGTH: 5
229 <212> TYPE: PRT
230 <213> ORGANISM: Artificial Sequence
W--> 231 <220> FEATURE:
232 <223> OTHER INFORMATION: Description of Artificial Sequence: synthesized
W--> 233 <400> SEQUENCE: 27
234 Gln Thr Ala Thr Lys
E--> 235 1 1 5 5

See
item #3
on error
summary
sheet.

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VERIFICATION SUMMARY

DATE: 06/02/2005

PATENT APPLICATION: US/10/049,967C

TIME: 08:23:11

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\06022005\J049967C.raw

L:3 M:283 W: Missing Blank Line separator, <120> field identifier
L:5 M:283 W: Missing Blank Line separator, <130> field identifier
L:6 M:283 W: Missing Blank Line separator, <140> field identifier
L:8 M:283 W: Missing Blank Line separator, <160> field identifier
L:10 M:283 W: Missing Blank Line separator, <210> field identifier
L:14 M:283 W: Missing Blank Line separator, <220> field identifier
L:16 M:283 W: Missing Blank Line separator, <400> field identifier
L:22 M:283 W: Missing Blank Line separator, <220> field identifier
L:24 M:283 W: Missing Blank Line separator, <400> field identifier
L:30 M:283 W: Missing Blank Line separator, <220> field identifier
L:32 M:283 W: Missing Blank Line separator, <400> field identifier
L:33 M:254 E: No. of Bases conflict, LENGTH:Input:29 Counted:28 SEQ:3 ✓
L:33 M:252 E: No. of Seq. differs, <211> LENGTH:Input:29 Found:28 SEQ:3 ✓
L:38 M:283 W: Missing Blank Line separator, <220> field identifier
L:40 M:283 W: Missing Blank Line separator, <400> field identifier
L:41 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:29 SEQ:4
L:41 M:252 E: No. of Seq. differs, <211> LENGTH:Input:30 Found:29 SEQ:4 ✓
L:46 M:283 W: Missing Blank Line separator, <220> field identifier
L:48 M:283 W: Missing Blank Line separator, <400> field identifier
L:49 M:254 E: No. of Bases conflict, LENGTH:Input:32 Counted:31 SEQ:5 ✓
L:49 M:252 E: No. of Seq. differs, <211> LENGTH:Input:32 Found:31 SEQ:5 ✓
L:54 M:283 W: Missing Blank Line separator, <220> field identifier
L:56 M:283 W: Missing Blank Line separator, <400> field identifier
L:62 M:283 W: Missing Blank Line separator, <220> field identifier
L:64 M:283 W: Missing Blank Line separator, <400> field identifier
L:70 M:283 W: Missing Blank Line separator, <220> field identifier
L:72 M:283 W: Missing Blank Line separator, <400> field identifier
L:78 M:283 W: Missing Blank Line separator, <220> field identifier
L:80 M:283 W: Missing Blank Line separator, <400> field identifier
L:86 M:283 W: Missing Blank Line separator, <220> field identifier
L:88 M:283 W: Missing Blank Line separator, <400> field identifier
L:94 M:283 W: Missing Blank Line separator, <220> field identifier
L:96 M:283 W: Missing Blank Line separator, <400> field identifier
L:102 M:283 W: Missing Blank Line separator, <220> field identifier
L:104 M:283 W: Missing Blank Line separator, <400> field identifier
L:110 M:283 W: Missing Blank Line separator, <220> field identifier
L:112 M:283 W: Missing Blank Line separator, <400> field identifier
L:118 M:283 W: Missing Blank Line separator, <220> field identifier
L:120 M:283 W: Missing Blank Line separator, <400> field identifier
L:126 M:283 W: Missing Blank Line separator, <220> field identifier
L:128 M:283 W: Missing Blank Line separator, <400> field identifier
L:134 M:283 W: Missing Blank Line separator, <220> field identifier
L:136 M:283 W: Missing Blank Line separator, <400> field identifier
L:142 M:283 W: Missing Blank Line separator, <220> field identifier
L:144 M:283 W: Missing Blank Line separator, <400> field identifier
L:150 M:283 W: Missing Blank Line separator, <220> field identifier
L:152 M:283 W: Missing Blank Line separator, <400> field identifier
L:158 M:283 W: Missing Blank Line separator, <220> field identifier

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DATE: 06/02/2005

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TIME: 08:23:11

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\06022005\J049967C.raw

L:160 M:283 W: Missing Blank Line separator, <400> field identifier
L:170 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:20 ✓
L:175 M:283 W: Missing Blank Line separator, <220> field identifier
L:177 M:283 W: Missing Blank Line separator, <400> field identifier
L:179 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:21 ✓
L:184 M:283 W: Missing Blank Line separator, <220> field identifier
L:186 M:283 W: Missing Blank Line separator, <400> field identifier
L:193 M:283 W: Missing Blank Line separator, <220> field identifier
L:195 M:283 W: Missing Blank Line separator, <400> field identifier
L:202 M:283 W: Missing Blank Line separator, <220> field identifier
L:226 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:26 ✓
L:235 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:27 ✓

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